ABSTRACT OF THE DISCLOSURE

In embodiments of the present invention, methods are provided for removing double-stranded oligonucleotide (*e.g.*, DNA) molecules containing one or more sequence errors, generated during nucleic acid synthesis, from a population of correct oligonucleotide duplexes. In one embodiment, the oligonucleotides are generated enzymatically. Heteroduplex (containing mismatched bases) oligonucleotides may be created by denaturing and reannealing the population of duplexes. The reannealed oligonucleotide duplexes are contacted with a mismatch recognition protein that interacts with (*e.g.*, binds and/or cleaves) the duplexes containing a base pair mismatch. The oligonucleotide heteroduplexes that have interacted with such a protein are separated, simultaneously with contacting or sequentially in a separate step, from homoduplexes. These methods are also used in another embodiment to remove heteroduplex oligonucleotides (*e.g.*, DNA) that are formed directly from chemical nucleic acid synthesis. In other embodiments of the present invention, kits and compositions useful for the methods are provided.